UNITED STATES PATENT AND TRADEMARK OFFICE

APPLICATION NO.	FILING DATE	FIRST NAMED INVENTOR	ATTORNEY DOCKET NO.	CONFIRMATION NO.
10/024,632	12/19/2001	Steve Sichuan He	38-21(51837)B	8916

7590	01/04/2006

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EXAMINER
BAUM, STUART F

ART UNIT	PAPER NUMBER
1638	

DATE MAILED: 01/04/2006

Please find below and/or attached an Office communication concerning this application or proceeding.

PTO-90C (Rev. 10/03)

-- The MAILING DATE of this communication appears on the cover sheet with the correspondence address --

Period for Reply

A SHORTENED STATUTORY PERIOD FOR REPLY IS SET TO EXPIRE <u>3</u> MONTH(S) OR THIRTY (30) DAYS, WHICHEVER IS LONGER, FROM THE MAILING DATE OF THIS COMMUNICATION.

- Extensions of time may be available under the provisions of 37 CFR 1.136(a). In no event, however, may a reply be timely filed after SIX (6) MONTHS from the mailing date of this communication.
- If NO period for reply is specified above, the maximum statutory period will apply and will expire SIX (6) MONTHS from the mailing date of this communication.
- Failure to reply within the set or extended period for reply will, by statute, cause the application to become ABANDONED (35 U.S.C. § 133). Any reply received by the Office later than three months after the mailing date of this communication, even if timely filed, may reduce any earned patent term adjustment. See 37 CFR 1.704(b).

Status

1) ☒ Responsive to communication(s) filed on *11 October 2005*.

2a) ☐ This action is **FINAL.**   2b) ☒ This action is non-final.

3) ☐ Since this application is in condition for allowance except for formal matters, prosecution as to the merits is closed in accordance with the practice under *Ex parte Quayle*, 1935 C.D. 11, 453 O.G. 213.

Disposition of Claims

4) ☒ Claim(s) *3-6* is/are pending in the application.

     4a) Of the above claim(s) _____ is/are withdrawn from consideration.

5) ☐ Claim(s) _____ is/are allowed.

6) ☒ Claim(s) *3-5* is/are rejected.

7) ☒ Claim(s) *6* is/are objected to.

8) ☐ Claim(s) _____ are subject to restriction and/or election requirement.

Application Papers

9) ☐ The specification is objected to by the Examiner.

10) ☒ The drawing(s) filed on *12/19/01, 5/6/02* is/are: a) ☒ accepted or b) ☐ objected to by the Examiner.

     Applicant may not request that any objection to the drawing(s) be held in abeyance. See 37 CFR 1.85(a).

     Replacement drawing sheet(s) including the correction is required if the drawing(s) is objected to. See 37 CFR 1.121(d).

11) ☐ The oath or declaration is objected to by the Examiner. Note the attached Office Action or form PTO-152.

Priority under 35 U.S.C. § 119

12) ☐ Acknowledgment is made of a claim for foreign priority under 35 U.S.C. § 119(a)-(d) or (f).

     a) ☐ All   b) ☐ Some * c) ☐ None of:

       1. ☐ Certified copies of the priority documents have been received.

       2. ☐ Certified copies of the priority documents have been received in Application No. _____.

       3. ☐ Copies of the certified copies of the priority documents have been received in this National Stage application from the International Bureau (PCT Rule 17.2(a)).

     * See the attached detailed Office action for a list of the certified copies not received.

Attachment(s)

1) ☒ Notice of References Cited (PTO-892)

2) ☐ Notice of Draftsperson's Patent Drawing Review (PTO-948)

3) ☐ Information Disclosure Statement(s) (PTO-1449 or PTO/SB/08) Paper No(s)/Mail Date _____.

4) ☐ Interview Summary (PTO-413) Paper No(s)/Mail Date. _____.

5) ☐ Notice of Informal Patent Application (PTO-152)

6) ☒ Other: *sequence search results*.

DETAILED ACTION

1.   In view of the appeal brief filed on 10/11/2005, PROSECUTION IS HEREBY

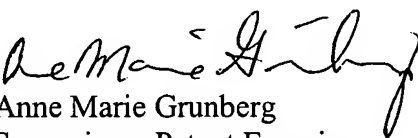REOPENED. New grounds of rejection are set forth below.

To avoid abandonment of the application, appellant must exercise one of the following

two options:

(1) file a reply under 37 CFR 1.111 (if this Office action is non-final) or a reply under 37

CFR 1.113 (if this Office action is final); or,

(2) initiate a new appeal by filing a notice of appeal under 37 CFR 41.31 followed by an

appeal brief under 37 CFR 41.37. The previously paid notice of appeal fee and appeal brief fee

can be applied to the new appeal. If, however, the appeal fees set forth in 37 CFR 41.20 have

been increased since they were previously paid, then appellant must pay the difference between

the increased fees and the amount previously paid.

A Supervisory Patent Examiner (SPE) has approved of reopening prosecution by signing

below:
Anne Marie Grunberg
Supervisory Patent Examiner
Art Unit 1638 and 1661

2.   Claims 3-6, including SEQ ID NO:2 are pending and are examined in the present office

action.

3.   The Office acknowledges Applicants' remarks in the Appeal Brief filed 10/11/2005, that

address the written description and enablement rejections from the final office action mailed

11/19/2004. Because the present written description, enablement and 102 rejections address new

issues, not previously before articulated, the Office holds off from addressing the remarks, and

will do so in the next office action, if appropriate.

Claim Objection

4.   Claims 6 is objected to for omitting the word "acid" after the word "amino". Correction

is requested.

Claim Rejections - 35 USC § 112

The following is a quotation of the second paragraph of 35 U.S.C. 112:

> The specification shall conclude with one or more claims particularly pointing out and distinctly claiming the
> subject matter which the applicant regards as his invention.

5.   Claim 4 is rejected under 35 U.S.C. 112, second paragraph, as being indefinite for failing

to particularly point out and distinctly claim the subject matter which applicant regards as the

invention.

Claim 4 is indefinite for reciting "stringent conditions". Applicants do not explicitly

define "stringent conditions" in the claims or in the specification (see page 17 of specification,

lines 14-29). Applicants only give examples of possible stringent hybridization conditions.

Therefore, the metes and bounds of "stringent conditions" have not been disclosed.

Written Description

The following is a quotation of the first paragraph of 35 U.S.C. 112:

> The specification shall contain a written description of the invention, and of the manner and process of making
> and using it, in such full, clear, concise, and exact terms as to enable any person skilled in the art to which it

> pertains, or with which it is most nearly connected, to make and use the same and shall set forth the best mode
> contemplated by the inventor of carrying out his invention.

6.   Claims 3-5 are rejected under 35 U.S.C. 112, first paragraph, as containing subject matter

which was not described in the specification in such a way as to reasonably convey to one skilled

in the relevant art that the inventor(s), at the time the application was filed, had possession of the

claimed invention.

The claims are drawn to an isolated nucleic acid molecule comprising a nucleic acid

sequence which encodes a polypeptide having an amino acid sequence that is substantially

identical to a sequence of SEQ ID NO:2, an isolated nucleic acid molecule comprising a

nucleotide sequence or its complement, which hybridizes under stringent conditions to a nucleic

acid molecule which encodes a protein with substantial identity to SEQ ID NO:2, or an isolated

nucleic acid sequence which encodes an amino acid sequence comprising SEQ ID NO:2

containing conservative amino acid substitutions.

Applicants define "substantially identical" and "substantial identity" to mean that one

amino acid or nucleotide sequence has 60% sequence identity when compared to a reference

amino acid or nucleotide sequence (page 15 of specification, lines 10-18).

The Office interprets "a sequence of SEQ ID NO:2" to read on a large number of

sequences because "a sequence of SEQ ID NO:2" reads on any two amino acids of SEQ ID

NO:2.

Because Applicants do not explicitly define "stringent conditions" in the claims or in the

specification (see page 17 of specification, lines 14-29) as noted above, the Office interprets

"stringent conditions" to mean low stringency conditions.

Applicants define "conservative amino acid substitutions" to mean substitutions of one or more amino acids in a native amino acid sequence with another amino acid(s) having similar side chains (page 15 of specification, lines 28-29).

Applicants isolated a cDNA clone from soybean, SEQ ID NO:1, that encodes SEQ ID NO:2, that shares sequence identity with the *Arabidopsis* ANT protein (pages 47-49, Example 1). Applicants disclose that SEQ ID NO:2 contains two AP2 DNA binding domains that share homology with the *Arabidopsis* ANT polypeptide, four conserved segments were identified in the N-terminal before the AP2 DNA binding domains, suggesting a possible functional role, and the C-terminal sequence of SEQ ID NO:2 bears little homology with that of the *Arabidopsis* ANT protein but does share conserved segments with another ANT-like clone isolated from soybean. Applicants suggest that these C-terminal segments may perform additional or distinguishable functions from the *Arabidopsis* ANT polypeptide (page 49, 2nd full paragraph).

The Applicants do not identify essential regions of SEQ ID NO:2 encoded by SEQ ID NO:1, nor do Applicants describe any polynucleotide sequence that encodes any protein comprising any two amino acids of SEQ ID NO:2, nor any polynucleotide sequence that encodes a protein exhibiting 60% amino acid identity with SEQ ID NO:2, nor any polynucleotide sequences that hybridize under low stringency conditions to another nucleotide sequence that encodes a protein having 60% amino acid identity to SEQ ID NO:2 nor any polynucleotide sequence encoding an amino acid sequence comprising SEQ ID NO:2 in which all amino acids have been substituted with conservative amino acids, and wherein the encoded protein has the same function/activity as the protein encoded by SEQ ID NO:1.

The Federal Circuit has recently clarified the application of the written description

requirement to inventions in the field of biotechnology. See University of California v. Eli Lilly

and Co., 119 F.3d 1559, 1568, 43 USPQ2d 1398, 1406 (Fed. Cir. 1997). In summary, the court

stated that a written description of an invention requires a precise definition, one that defines the

structural features of the chemical genus that distinguishes it from other chemical structures. A

definition by function does not suffice to define the genus because it is only an indication of

what the gene does, rather than what it is. The court goes on to say, "A description of a genus of

cDNAs may be achieved by means of a recitation of a representative number of cDNAs, defined

by nucleotide sequence, falling within the scope of the genus or of a recitation of structural

features common to members of the genus, which features constitute a substantial portion of the

genus." *See University of California v. Eli Lilly and Co.*, 119 F.3d 1559; 43 USPQ2d 1398,

1406 (Fed. Cir. 1997).

Applicants fail to describe a representative number of polynucleotide sequences encoding

SEQ ID NO:2 falling within the scope of the claimed genus of polynucleotides, comprising

sequences that encode polypeptides that comprise any two amino acids of SEQ ID NO:2, or

encode a polypeptide exhibiting 60% amino acid identity with SEQ ID NO:2, or polynucleotides

that hybridize under low stringency conditions with another polynucleotide that encodes a

polypeptide exhibiting 60% sequence identity with SEQ ID NO:2, or a polynucleotide which

encodes a polypeptide comprising SEQ ID NO:2 in which all of the amino acids have been

substituted with conservative amino acids, and wherein any of the encoded proteins have the

same function/activity as the protein encoded by SEQ ID NO:1. Applicants only describe a

single cDNA of SEQ ID NO:1 encoding SEQ ID NO:2. Furthermore, Applicants fail to describe

structural features common to members of the claimed genus of polynucleotides. Hence,

Applicants fail to meet either prong of the two-prong test set forth by *Eli Lilly*. Furthermore,

given the lack of description of the necessary elements essential for the protein of SEQ ID NO:2,

it remains unclear what features identify the genus of nucleic acid sequences encoding the

claimed genus of polypeptides. Since the genus of proteins of SEQ ID NO:2 has not been

described by specific structural features, the specification fails to provide an adequate written

description to support the breath of the claims.

Scope of Enablement

7.   Claims 3-5 are rejected under 35 U.S.C. 112, first paragraph, because the specification,

while being enabling for an isolated nucleic acid molecule comprising a nucleotide sequence

encoding the amino acid sequence comprising SEQ ID NO:2, does not reasonably provide

enablement for a nucleotide sequence or its complement, which encode a polypeptide having an

amino acid sequence that is substantially identical to a sequence of SEQ ID NO:2, an isolated

nucleic acid molecule comprising a nucleotide sequence or its complement, which can hybridize

under stringent conditions to a nucleic acid sequence which can encode a protein with substantial

identity to SEQ ID NO:2, or an isolated nucleic acid sequence which encodes an amino acid

sequence comprising SEQ ID NO:2 containing conservative amino acid substitutions. The

specification does not enable any person skilled in the art to which it pertains, or with which it is

most nearly connected, to make and/or use the invention commensurate in scope with these

claims.

The claimed invention is not supported by an enabling disclosure taking into account the

Wands factors. *In re Wands,* 858/F.2d 731, 8 USPQ2d 1400 (Fed. Cir. 1988). *In re Wands* lists

a number of factors for determining whether or not undue experimentation would be required by

one skilled in the art to make and/or use the invention. These factors are: the quantity of

experimentation necessary, the amount of direction or guidance presented, the presence or

absence of working examples of the invention, the nature of the invention, the state of the prior

art, the relative skill of those in the art, the predictability or unpredictability of the art, and the

breadth of the claim.

The claims are drawn to an isolated nucleic acid molecule comprising a nucleotide

sequence or its complement, which encode a polypeptide having an amino acid sequence that is

substantially identical to a sequence of SEQ ID NO:2, an isolated nucleic acid molecule

comprising a nucleotide sequence or its complement, which can hybridize under stringent

conditions to a nucleic acid sequence which can encode a protein with substantial identity to

SEQ ID NO:2, or an isolated nucleic acid sequence which encodes an amino acid sequence

comprising SEQ ID NO:2 containing conservative amino acid substitutions.

Applicants define "substantially identical" and "substantial identity" to mean that one

amino acid or nucleotide sequence has 60% sequence identity when compared to a reference

amino acid or nucleotide sequence (page 15 of specification, lines 10-18).

The Office interprets "a sequence of SEQ ID NO:2" to read on a large number of

sequences because "a sequence of SEQ ID NO:2" reads on any two amino acids of SEQ ID

NO:2.

Because Applicants do not explicitly define "stringent conditions" in the claims or in the specification (see page 17 of specification, lines 14-29) as noted above, the Office interprets "stringent conditions" to mean low stringency conditions.

Applicants define "conservative amino acid substitutions" to mean substitutions of one or more amino acids in a native amino acid sequence with another amino acid(s) having similar side chains (page 15 of specification, lines 28-29).

Applicants isolated a cDNA clone from soybean, SEQ ID NO:1, that encodes SEQ ID NO:2, that shares sequence identity with the *Arabidopsis* ANT protein (pages 47-49, Example 1). Applicants disclose that SEQ ID NO:2 contains two AP2 DNA binding domains that share homology with the *Arabidopsis* ANT polypeptide, four conserved segments were identified in the N-terminal before the AP2 DNA binding domains, suggesting a possible functional role, and the C-terminal sequence of SEQ ID NO:2 bears little homology with that of the *Arabidopsis* ANT protein but does share conserved segments with another ANT-like clone isolated from soybean. Applicants suggest that these C-terminal segments may perform additional or distinguishable functions from the *Arabidopsis* ANT polypeptide (page 49, 2nd full paragraph). Applicants transformed *Arabidopsis* with SEQ ID NO:1 operably linked to the 35S promoter to produce plants with increased growth and biomass of the roots (page 72, 1st paragraph), increased floral size and increased seed size (page 73, Examples 28 and 29).

Applicants are not enabled for the full scope of the broadly claimed invention. Applicants have not disclosed any nucleotide sequence that encodes a protein exhibiting 60% amino acid identity with SEQ ID NO:2 or with any sequence disclosed in SEQ ID NO:2 and can be used to transform a plant in which the resultant transgenic plant phenotype is the same as a

plant transformed with a nucleic acid encoding SEQ ID NO:2. Applicants have also not

disclosed a nucleotide sequence or its complement, which hybridizes under low stringency

conditions to a nucleotide sequence encoding a protein exhibiting 60% amino acid identity with

SEQ ID NO:2, and wherein a plant transformed with said nucleotide sequence results in a plant

phenotype that is the same as a plant transformed with a nucleic acid encoding SEQ ID NO:2.

And lastly, Applicants have not disclosed a nucleic acid sequence which encodes a protein

comprising SEQ ID NO:2 in which every amino acid has been substituted with a corresponding

conservative amino acid, and wherein a plant transformed with said nucleic acid exhibits a

phenotype that is the same as a plant transformed with a nucleic acid encoding SEQ ID NO:2.

The state-of-the-art is such that one of skill in the art cannot predict which nucleic acids

that encode a polypeptide with substantial identity to SEQ ID NO:2 will encode a protein with

the same activity as a protein comprising the amino acid sequence of SEQ ID NO:2. The

prediction of protein structure from sequence data and, in turn, utilizing predicted structural

determinations to ascertain functional aspects of the protein, is extremely complex, and the

positions within the protein's sequence where amino acid substitutions can be made with a

reasonable expectation of maintaining function are limited (Bowie et al, Science 247:1306-1310,

1990, see especially page 1306). Proteins may be sensitive to alterations in even a single amino

acid in a sequence. For example, the replacement of a glycine residue located within the START

domain of either the PHABULOSA or PHAVOLUTA protein receptor with either an alanine or

aspartic acid residue, alters the sterol/lipid binding domain (McConnell et al, Nature 411

(6838):709-713, 2001, see especially page 710, left column, 2nd paragraph).

Making "conservative" substitutions (*e.g.*, substituting one polar amino acid for another, or one acidic one for another) does not produce predictable results. Lazar et al (1988, Mol. Cell. Biol. 8:1247-1252) showed that the "conservative" substitution of glutamic acid for aspartic acid at position 47 reduced biological function of transforming growth factor alpha while "nonconservative" substitutions with alanine or asparagine had no effect (abstract). Similarly, Hill et al (1998, Biochem. Biophys. Res. Comm. 244:573-577) teach when three histidines that are maintained in ADP-glucose pyrophosphorylase across several species are substituted with the "nonconservative" amino acid glutamine, there is little effect on enzyme activity, while the substitution of one of those histidines with the "conservative" amino acid arginine drastically reduced enzyme activity (see Table 1). All these mutated proteins, would produce a polypeptide with substantial identity with SEQ ID NO:2. The nucleic acids encoding all these mutated proteins, however, would hybridize under stringent conditions to the nucleic acids encoding the original protein.

Applicants' claims are drawn to nucleic acid sequences that hybridize to a nucleic acid sequence encoding a polypeptide with substantial identity to SEQ ID NO:2, but the state-of-the-art teaches isolating DNA fragments using stringent hybridization conditions, does not always select for DNA fragments whose contiguous nucleotide sequence is the same or nearly the same as the probe. Fourgoux-Nicol et al (1999, Plant Molecular Biology 40 :857-872) teach the isolation of a 674bp fragment using a 497bp probe incorporating stringent hybridization conditions comprising three consecutive 30 minute rinses in 2X, 1X and 0.1X SSC with 0.1% SDS at $65^{0}C$ (page 859, left column, 2nd paragraph). Fourgoux-Nicol et al also teach that the probe and isolated DNA fragment exhibited a number of sequence differences comprising a 99bp

insertion and a single nucleotide gap, while the DNA fragment contained 2 single nucleotide

gaps and together the fragments contained 27 nucleotide mismatches. Taking into account the

insertions, gaps and mismatches, the longest stretch of contiguous nucleotides to which the probe

could hybridize consisted of 93bp of DNA (page 862, Figure 2).

Given the Office's interpretation of "a sequence of SEQ ID NO:2" as discussed above,

the state-of-the-art teaches transforming a plant with a nucleic acid sequence that encodes a

polypeptide that is substantially identical to any sequence of SEQ ID NO:2 produces unexpected

results. Kano-Murakami et al (1993, FEBS 334:365-368) teach introducing the *Oryza sativa*

homeobox 1 (OSH1) gene into tobacco. OSH1 is a rice homologue of the *Knotted-1* homeobox

gene from maize and would be encompassed by Applicant's broad claim language, as discussed

above. Kano-Murakami et al teach transgenic tobacco plants comprising the OSH1 gene display

a "range of phenotypes which include abnormalities in leaf and petal shape as well as stem

height and number" (page 365, right column, 1st paragraph).

Applicants have not disclosed how one makes or isolates any of the sequences that are

encompassed by Applicants' broad claims. Applicants have not taught which regions of the

respective polynucleotides can be used to amplify any of said polynucleotides or which regions

can be used as a probe to isolate any of said polynucleotide sequences.

In the absence of guidance, undue trial and error experimentation would be required for

one of ordinary skill in the art to screen through the multitude of non-exemplified sequences,

either by selecting random pieces of DNA as probes or by designing primers to undisclosed

regions of SEQ ID NO:2 and isolating or amplifying fragments, subcloning the fragments,

producing expression vectors and transforming plants therewith, in order to identify those, if any,

that when over-expressed could produce plants with a morphology as specified by Applicant and encode a protein with substantial identity to a sequence of SEQ ID NO:2, or wherein the nucleotide sequence or its complement can hybridizes under low stringency conditions to a nucleotide sequence encoding a protein exhibiting 60% amino acid identity with SEQ ID NO:2, or wherein the nucleic acid sequence can encodes a protein comprising SEQ ID NO:2 in which every amino acid has been substituted with a corresponding conservative amino acid.

Therefore, given the breadth of the claims; the lack of guidance and examples; the unpredictability in the art; and the state-of-the-art as discussed above, undue experimentation would be required to practice the claimed invention, and therefore the invention is not enabled.

Claim Rejections - 35 USC § 102

(b) the invention was patented or described in a printed publication in this or a foreign country or in public use or on sale in this country, more than one year prior to the date of application for patent in the United States.

8. Claims 3-5 are rejected under 35 U.S.C. 102(b) as being anticipated by Elliott et al (1996, The Plant Cell 8:155-168).

The claims are drawn to an isolated nucleic acid molecule comprising a nucleotide sequence, or its complement which encodes a polypeptide having an amino acid sequence that is substantially identical to a sequence of SEQ ID NO:2, an isolated nucleic acid molecule comprising a nucleotide sequence, or its complement, which hybridizes under stringent conditions to a nucleic acid molecule which encodes a protein with substantial identity to SEQ ID NO:2, or an isolated nucleic acid sequence which encodes an amino acid sequence comprising SEQ ID NO:2 containing conservative amino acid substitutions.

Applicants define "substantially identical" and "substantial identity" to mean that one amino acid or nucleotide sequence has 60% sequence identity when compared to a reference amino acid or nucleotide sequence (page 15 of specification, lines 10-18).

The Office interprets "a sequence of SEQ ID NO:2" to read on a large number of sequences because "a sequence of SEQ ID NO:2" reads on any two amino acids of SEQ ID NO:2.

Because Applicants do not explicitly define "stringent conditions" in the claims or in the specification (see page 17 of specification, lines 14-29) as noted above, the Office interprets "stringent conditions" to mean low stringency conditions.

Applicants define "conservative amino acid substitutions" to mean substitutions of one or more amino acids in a native amino acid sequence with another amino acid(s) having similar side chains (page 15 of specification, lines 28-29).

Elliott et al teach a nucleic acid sequence that encodes the Arabidopsis AINTEGUMENTA (ANT) protein that exhibits 38% sequence identity to Applicants' SEQ ID NO:2 (See enclosed sequence search results). The sequence of Elliot et al encodes a protein that is substantially identical to any sequence of SEQ ID NO:2, given that the encoded protein comprises at least any two amino acid residues that are found in Applicants' encoded protein. The sequence of Elliot et al would hybridize under low stringency conditions to a nucleic acid sequence encoding a protein exhibiting 60% amino acid identity to SEQ ID NO:2. Lastly, the Office considers the nucleic acid sequence of Elliot et al to encode a polypeptide comprising SEQ ID NO:2 containing conservative amino acid substitutions because the Office considers all amino acids that are not 100% identical to the respective amino acids in applicants' SEQ ID

NO:2, to be amino acids comprising similar side chains, based on applicants' definition of

"conservative amino acid substitutions" as disclosed above. And as such, Elliot et al anticipate

the claimed invention.

9.   Claim 6 is deemed free of the prior art, given the failure of the prior art to teach or

reasonably suggest an isolated nucleic acid sequence encoding the amino acid sequence

comprising SEQ ID NO:2.

10.   Claim 6 is objected to, but would be allowable if rewritten to correct the deficiencies as

discussed above.
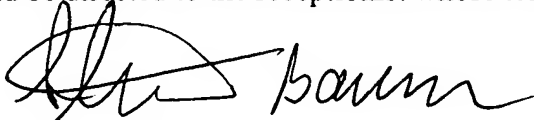
11.   Claims 3-5 are not allowed.

12.   Any inquiry concerning this communication or earlier communications from the

examiner should be directed to Stuart F. Baum whose telephone number is 571-272-0792. The

examiner can normally be reached on M-F 8:30-5:00.

        If attempts to reach the examiner by telephone are unsuccessful, the examiner's

supervisor, Anne Marie Grunberg can be reached at 571-272-0975. The fax phone number for

the organization where this application or proceeding is assigned is 571-273-8300.

Any inquiry of a general nature or relating to the status of this application or proceeding

should be directed to the receptionist whose telephone number is 571-272-1600.

Stuart F. Baum Ph.D.
Patent Examiner
Art Unit 1638
December 19, 2005

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RESULT 8
ATU41339
LOCUS          ATU41339
DEFINITION     Arabidopsis thaliana ANT (AINTEGUMENTA) mRNA, complete cds.
ACCESSION      U41339
VERSION        U41339.1  GI:1244707
KEYWORDS       .
SOURCE         Arabidopsis thaliana (thale cress)
ORGANISM       Arabidopsis thaliana
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REFERENCE      1  (bases 1 to 1905)
AUTHORS        Elliott,R.C., Betzner,A.S., Huttner,E., Oakes,M.P., Tucker,W.Q.,
               Gerentes,D., Perez,P. and Smyth,D.R.
TITLE          AINTEGUMENTA, an APETALA2-like gene of Arabidopsis with pleiotropic
               roles in ovule development and floral organ growth
JOURNAL        Plant Cell 8 (2), 155-168 (1996)
MEDLINE        96351414
PUBMED         8742707
REFERENCE      2  (bases 1 to 1905)
AUTHORS        Smyth,D.R.
TITLE          Direct Submission
JOURNAL        Submitted (27-NOV-1995) David Smyth, Genetics and Dev. Biology,
               Monash University, Wellington Road, Clayton, VIC 3168, Australia
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ORIGIN

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Mismatches:                 37.92%
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Matches:       312
Conservative:  69
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Gaps:          21

DB:

US-10-024-632-2 (1-663) x ATU41339 (1-1905)

Qy     1 MetLysArgIleAsnGluSerAsnAsnThrAspAspGlyAsnAsnHisAsnTrpLeuGly    20
           ::::::::::::: ::::: :::::::           ||| |||||  ::|||||
Db    38 ATGAAGTCTTTTGTGATAATGATGATAATAATCATAGCAACGACGACTAATTTGTTAGGG    97

Qy    21 PheSerLeuSerProHis---MetLysMet                                29
         |||||||||| ::|||::     |||||||
Db    98 TTCTCATTGTCTTCAAATATGATGAAAATGGGAGGAGTAGAGAAGCTAGAGAAGCTATTAC   157

Qy    30 ---------------GluAlaThrSerAlaAlaThrValProThrThrPheTyrMet      43
                         :::||::::|::
Db   158 TCATCTTCAACTTCTTCAGCTGCAACTTCTCTTCCTCGTTCCACCTCAACTGTGTT       217

Qy    44 SerProSerGlnSerHisLeuSerAsnPheGlyMetCysTyrGlyValGlyValAsnGly    63
                   ||| |||:: ::  ||||||||::::::|||||::::|||
Db   218 GGT-----------GACAACACTGGTGTTGGTGTTGGTCTATGGATCCAACCCAAATGGA   268

Qy    64 AsnPheHisSerProLeuThrValMetProLeuLysSerAspGlySerLeuCysIleLeu    83
           :::::::||:::::||:::||||::::||||||||||||||||:::|||
Db   269 GGAATCTATTCTCACATGTCTGTGATGCCACTCAAGATCTGATGGTTCCTTTGCTTAATG   328

Qy    84 GluAlaLeuLysArgSerGlnThrGlnValMetValProThrSerProLysLeuGlu    103
         |||||||||||:::||:||:::||||||||||||||::||:::|||
Db   329 GAAGCTCTCAACAGATCCTCTCCACTCGAATCACCATCAAGATTCATCCCAAAGGTGGAG   388

Qy   104 AspPheLeuGlyGlyAlaThrMetGlyThrHisGluTyrGlySerHisGluArgGly--   122
         ||::||     ||::|||||:::::
Db   389 GATTTCTTTGGG------ACCATCACAACAACACAGTCAAAGAGAGCCATG          436

Qy   123 ---LeuSerLeuAspSerIleTyrTyrAsnSerGlnAsnAlaGluAlaGlnProAsnArg   141
             |||  |||||| :||:|||||
Db   437 GATCTTAGCTTAGATAGTTTATTCTACAACACCACTCAT---------GAGCCCAACACG   487

Qy   142 AspLeuLeuSerGlnProPhe----------ArgGlnGlnGlyHisMetSerValGln   157
         ||| |||            |||     :::  :::
Db   488 ACTACAAACTTCAAGAGTTCTTAGCTTCCCTCAAACCAGAAACCAT-----------   535

Qy   158 ThrHisProTyrTyrSerGlyLeuAlaCysHisGlyLeuTyrGlnAlaProLeuGluGlu   177
         ||| |||
Db   536 ----------------------------------------------GAGGAA   541

Qy   178 GluThrThrLysGluThrHisValSerAspCysSerSerLeuMetProGlnMetThrGlu   197
         ||::||       ::: ::|||
Db   542 GAAACT------AGAAATTACGGGAATGAC--------CCTAGTTGACACAT           580

Qy   198 GlyLeuLysAsnTrpValAlaProThrArgGluPheSerThrHisGlnIleValLeuGlu   217
         |||
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Qy   546 IleMetAsnCysGlyAsnTyrArgAsnSerAlaPheSerMetAlaLeuGlnAspLeuIle 565

Db  1478 GCTCTAAATGCT---------------------- 1489

Qy   566 GlyIleAspSerValGlySerGlyGlnHisAsnMetLeuAspGluSerLysIleGly 585

Db  1489 ---------------------------------- 1489

Qy   586 ThrHisPheSerAsnThrSerSerLeuValThrSerLeuSerSerArgGluAlaSer 605
                                              |||
Db  1490 ----------------------GTTGTGGAAGGTGGTTCCAACAAGAAGTCAGT 1522

Qy   606 ProGluLysArgGlyProSerLeu-----LeuPheProMetProProMetGluThrLys 623
              ::|:||
Db  1523 ACTCCCGAGAGACTCTTGAGTTTTCCGGCGATTTTCCGGGTTGCCTCAAGTTAATCAAAG 1582

Qy   624 IleVal--AsnProIleGlyThrSerValThrSerTrpLeuProSerProThrValGln 642
              :::      :::|||||
Db  1583 ATGTTCGGATCAAATATGGGCGGAAATATGAGTCCTTGGACATCAAACCCTAATGCTCAG 1642

Qy   643 MetArgProSerProAlaIleSerLeuSerHisLeuProValPheAlaSerTrpThrAsp 662
              :::|||
Db  1643 CTTAAG---ACCGTCGCTCTTACTTTGCCTCAGATGCCCGGTTTTCGCTGCTTGGGCTGAT 1699

Qy   663 Thr 663
              :::
Db  1700 TCT 1702
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RESULT 9

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Db   581 GGA-------------------- 583

Qy   218 GlnGlnMetAsnCysGlyMetGlyArgGluArgAsnGlyValSerLeuGlySerValGly 237
              |||  ::|::|   |||
Db   584 GGGTCTTTAATGTAGGGGTATATGGGGAATTCAA------- 619

Qy   238 CysGlyGluLeuGlnSerLeuSerMetSerProGlySerGlnSerSerCysVal 257
              |||||||||||||||||||||||||||||||:::
Db   620 ---------CAGTCACTGAGCTTATCCATGAGCCCTGGGTCACAATCTAGCTGCATC 667

Qy   258 ThrAlaProSer------- 261
              |||
Db   668 ACTGGGCTCTCACCACCACCAACAAAACCAAAACCACCAAAGCCAAAACCACCAG 727

Qy   262 ------------------GlyThrAspSerValAlaVal 268
Db   728 CAGATCTCTGAGCTCTTGTGGAGACAAGCGTTGGGTTGAGACCGACACAATGGCCGGCT 787

Qy   269 AspAlaLysGlyLysArgGlyHis--------AlaLysLeuGlyLysGlnLysGlnProValHis 285
              :::|||||||||||||
Db   788 GCCAAGAAGAGAGAGGGGACAAGAGGACGATGTTGTAGTTGTTGGTCAGAAACAGATTGTTCAT 847

Qy   286 ArgLysSerIleLeuAspThrPheGlyGlnArgThrSerGlnTyrArgGlyValThrArgHis 305
              |||||||||||||||||||||||||||||||
Db   848 AGAAAATCATCGATACTTTGACAACAGAACTTCTCAATACCGAGGGCCGTACAAGACAT 907

Qy   306 ArgTrpThrGlyArgTyrGluAlaHisLeuTrpAspAsnSerCysLysLysGluGlyGln 325
              |||||||||||||||||||||||||||||||
Db   908 AGATGGACACGGTAGAATATGAAGCCTCATCATCGGACAATAGTTCAAGAAGGAAGGTCAC 967

Qy   326 ThrArgLysGlyArgGlnValTyrLeuGlyGlyTyrAspMetGluGluLysAlaAlaArg 345
              ::|||||||||||||||||||||||||||||||||||||
Db   968 AGTAGAAAAAGGAAGACAAGTTTATCTCGGAGGTTATGATATGGAGGAGAAAGCTGCTCGA 1027

Qy   346 AlaTyrAspLeuAlaAlaLeuLysTyrTyrTrpGlyProSerThrHisIleAsnPheSerIle 365
              |||||||||||||||||||||||||||||||||||||
Db  1028 GCATATGATCTTGCTGCACTCAAGTACTACTGGGGTCCCTCTACTCACCAGAATTTCTCTGCG 1087

Qy   366 GluAsnTyrGlnInValGlnLeuGlnLysMetLysGluAsnMetSerArgGlnGluThrTyrValAla 385
              |||||::|||||||||||||||||||||||||||||
Db  1088 GAGAATTATCAGAAACAGAATGAAGACATGAGCAGACATGAGCAAGAAATATGTTGCA 1147

Qy   386 HisLeuArgArgLysSerSerGlyPheSerArgGlyAlaSerIleTyrArgGlyValThr 405
              |||||||||||||||||||||||||||||||||||||
Db  1148 CATTTGAGAAGGAAGAGCCAGTGGTTTCTCTAGGGGTGCTTCCATCATACAGAGGAGTCACA 1207

Qy   406 ArgHisHisGlnHisGlyArgTrpGlnAlaArgIleGlyArgValAlaAlaGlyAsnLysAsp 425
              |||||||||||||||||||||||||||||||||||||
Db  1208 AGACATCACCAGCATGGAAGGTGGCAAGCACGGATTGGTAGAGTCGGTCGGAAACAAAGAT 1267

Qy   426 LeuTyrLeuGlyThrPheSerThrGluGluAlaAlaAlaGluAlaTyrAspValAlaAlaAla 445
              |||||||||||||||||||||||||||||||||||||
Db  1268 CTCTACCTTGGAACTTTCGGAACCCAAGAAGAAGCTGCAGAAGCTTACGATGTAGCAGCA 1327

Qy   446 IleLysPheArgGlyAlaAspAlaValThrPheAsnPheAspIleSerArgTyrAspSerGlu 465
              |||||||||||||||||||||||||||::|||
Db  1328 ATTAAGTTCCGTGGCACAAATGCTGTGACTAACTTTGATATCACGAGGTACGATGTTGAT 1387

Qy   466 ArgIleMetAlaSerSerAsnLeuLeuAlaGlyGluLeuAlaArgAlaArgLysAspAspAsn 485
              ::|||||:|||:|:|::
Db  1388 CGTATCATGTCAGTAACACCACTCTGTCTGGAGAGTTAGCCGCAAGGAAC-------- 1438

Qy   486 AspProArgAsnLysAspIleAspTyrAsnLysSerValThrSerValAlaAsnAsnGlu 505
              |||
Db  1439 -----------AACAACAGCATTGTC-------GTCAGGAATACT 1465

Qy   506 GluThrValGlnValGlnAlaGlyLysAsnAlaAsnAsnGluAsnAspSerGluTrpLysMet 525
              |||
Db  1466 GAA--------- 1468

Qy   526 ValLeuPheAsnHisProSerGlnGlnInGlnInAlaAsnGlyAsnGlySerAspGlnLys 545
              |||
Db  1469 -----------------GACCAAACC 1477
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